



#12/B

1/10

SEQUENCE LISTING

<110> Chen, Li How
Meade, Henry

<120> NOVEL MODIFIED MSP-1 NUCLEIC ACID SEQUENCES AND METHODS
FOR INCREASING mRNA LEVELS AND PROTEIN EXPRESSIONS IN
CELL SYSTEMS

<130> 10275/134001

<140> US 09/175,683

<141> 1998-10-20

<150> US 60/095,649

<151> 1998-08-07

<150> US 60/062,592

<151> 1997-10-20

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1065

<212> DNA

<213> preferably, a bacterium, virus, or parasite

<220>

<221> CDS

<222> (1)...(1065)

<400> 1

gcc gtc act ccc tcc gtc atc gat aac atc ctg tcc aag atc gag aac 48
Ala Val Thr Pro Ser Val Ile Asp Asn Ile Leu Ser Lys Ile Glu Asn
1 5 10 15

gag tac gag gtg ctg tac ctg aag ccg ctg gca ggg gtc tac cgg agc 96
Glu Tyr Glu Val Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser
20 25 30

ctg aag aag cag ctg gag aac aac gtg atg acc ttc aac gtg aac gtg 144
Leu Lys Lys Gln Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val
35 40 45

aag gat atc ctg aac agc cgg ttc aac aag cgg gag aac ttc aag aac 192
Lys Asp Ile Leu Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn
50 55 60

gtg ctg gag agc gat ctg atc ccc tac aag gat ctg acc agc agc aac 240
Val Leu Glu Ser Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn
65 70 75 80

tac gtg gtc aag gat ccc tac aag ttc ctg aac aag gag aag aga gat 288
Tyr Val Val Lys Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp
85 90 95

aag ttc ctg agc agt tac aac tac atc aag gat agc att gat acc gat 336
Lys Phe Leu Ser Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp
100 105 110

atc aac ttc gcc aac gat gtc ctg gga tac tac aag atc ctg tcc gag 384
 Ile Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu
 115 120 125

aag tac aag agc gat ctg gat tca atc aag aag tac atc aac gat aag 432
 Lys Tyr Lys Ser Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys
 130 135 140

cag gga gag aac gag aag tac ctg ccc ttc ctg aac aac atc gag acc 480
 Gln Gly Glu Asn Glu Lys Tyr Leu Pro Phe Leu Asn Asn Ile Glu Thr
 145 150 155 160

ctg tac aag acc gtc aac gat aag att gat ctg ttc gtg atc cac ctg 528
 Leu Tyr Lys Thr Val Asn Asp Lys Ile Asp Leu Phe Val Ile His Leu
 165 170 175

gag gcc aag gtc ctg aac tac aca tat gag aag agc aac gtg gag gtc 576
 Glu Ala Lys Val Leu Asn Tyr Thr Tyr Glu Lys Ser Asn Val Glu Val
 180 185 190

aag atc aag gag ctg aat tac ctg aag acc atc cag gat aag ctg gcc 624
 Lys Ile Lys Glu Leu Asn Tyr Leu Lys Thr Ile Gln Asp Lys Leu Ala
 195 200 205

gat ttc aag aag aac aac aac ttc gtc ggg atc gcc gat ctg agc acc 672
 Asp Phe Lys Lys Asn Asn Asn Phe Val Gly Ile Ala Asp Leu Ser Thr
 210 215 220

gat tac aac cac aac aac ctg ctg acc aag ttc ctg agc acc ggt atg 720
 Asp Tyr Asn His Asn Asn Leu Leu Thr Lys Phe Leu Ser Thr Gly Met
 225 230 235 240

gtc ttc gaa aac ctg gcc aag acc gtc ctg agc aac ctg ctg gat ggg 768
 Val Phe Glu Asn Leu Ala Lys Thr Val Leu Ser Asn Leu Leu Asp Gly
 245 250 255

aac ctg cag ggg atg ctg aac atc agc cag cac cag tgt gtg aag aag 816
 Asn Leu Gln Gly Met Leu Asn Ile Ser Gln His Gln Cys Val Lys Lys
 260 265 270

cag tgt ccc cag aac agc ggg tgt ttc aga cac ctg gat gag aga gag 864
 Gln Cys Pro Gln Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu
 275 280 285

gag tgt aag tgt ctg ctg aac tac aag cag gaa ggt gat aag tgt gtg 912
 Glu Cys Lys Cys Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val
 290 295 300

gaa aac ccc aat cct act tgt aac gag aac aat ggt gga tgt gat gcc 960
 Glu Asn Pro Asn Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala
 305 310 315 320

gat gcc aag tgt acc gag gag gat tca ggg agc aac ggg aag aag atc 1008
 Asp Ala Lys Cys Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile
 325 330 335

acc tgt gag tgt acc aag cct gat tct tat cca ctg ttc gat ggt atc 1056
 Thr Cys Glu Cys Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile
 340 345 350

B1
 cont.

ttc tgt agt
Phe Cys Ser
355

1065

<210> 2

<211> 1088

<212> DNA

<213> preferably, a bacterium, virus, or parasite

<220>

<221> CDS

<222> (1)...(1083)

<400> 2

| | |
|---|----|
| gca gta act cct tcc gta att gat aac ata ctt tct aaa att gaa aat | 48 |
| Ala Val Thr Pro Ser Val Ile Asp Asn Ile Leu Ser Lys Ile Glu Asn | |
| 1 5 10 15 | |

| | |
|---|----|
| gaa tat gag gtt tta tat tta aaa cct tta gca ggt gtt tat aga agt | 96 |
| Glu Tyr Glu Val Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser | |
| 20 25 30 | |

| | |
|---|-----|
| tta aaa aaa caa tta gaa aat aac gtt atg aca ttt aat gtt aat gtt | 144 |
| Leu Lys Lys Gln Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val | |
| 35 40 45 | |

| | |
|---|-----|
| aag gat att tta aat tca cga ttt aat aaa cgt gaa aat ttc aaa aat | 192 |
| Lys Asp Ile Leu Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn | |
| 50 55 60 | |

| | |
|---|-----|
| gtt tta gaa tca gat tta att cca tat aaa gat tta aca tca agt aat | 240 |
| Val Leu Glu Ser Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn | |
| 65 70 75 80 | |

| | |
|---|-----|
| tat gtt gtc aaa gat cca tat aaa ttt ctt aat aaa gaa aaa aga gat | 288 |
| Tyr Val Val Lys Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp | |
| 85 90 95 | |

| | |
|---|-----|
| aaa ttc tta agc agt tat aat tat att aag gat tca ata gat acg gat | 336 |
| Lys Phe Leu Ser Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp | |
| 100 105 110 | |

| | |
|---|-----|
| ata aat ttt gca aat gat gtt ctt gga tat tat aaa ata tta tcc gaa | 384 |
| Ile Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu | |
| 115 120 125 | |

| | |
|---|-----|
| aaa tat aaa tca gat tta gat tca att aaa aaa tat atc aac gac aaa | 432 |
| Lys Tyr Lys Ser Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys | |
| 130 135 140 | |

| | |
|---|-----|
| caa ggt gaa aat gag aaa tac ctt ccc ttt tta aac aat att gag acc | 480 |
| Gln Gly Glu Asn Glu Lys Tyr Leu Pro Phe Leu Asn Asn Ile Glu Thr | |
| 145 150 155 160 | |

| | |
|---|-----|
| tta tat aaa aca gtt aat gat aaa att gat tta ttt gta att cat tta | 528 |
| Leu Tyr Lys Thr Val Asn Asp Lys Ile Asp Leu Phe Val Ile His Leu | |
| 165 170 175 | |

Cont.

4/10

| | |
|---|------|
| gaa gca aaa gtt cta aat tat aca tat gag aaa tca aac gta gaa gtt Glu Ala Lys Val Leu Asn Tyr Thr Tyr Glu Lys Ser Asn Val Glu Val 180 185 190 | 576 |
| aaa ata aaa gaa ctt aat tac tta aaa aca att caa gac aaa ttg gca Lys Ile Lys Glu Leu Asn Tyr Leu Lys Thr Ile Gln Asp Lys Leu Ala 195 200 205 | 624 |
| gat ttt aaa aaa aat aac aat ttc gtt gga att gct gat tta tca aca Asp Phe Lys Lys Asn Asn Asn Phe Val Gly Ile Ala Asp Leu Ser Thr 210 215 220 | 672 |
| gat tat aac cat aat aac tta ttg aca aag ttc ctt agt aca ggt atg Asp Tyr Asn His Asn Asn Leu Leu Thr Lys Phe Leu Ser Thr Gly Met 225 230 235 240 | 720 |
| gtt ttt gaa aat ctt gct aaa acc gtt tta tct aat tta ctt gat gga Val Phe Glu Asn Leu Ala Lys Thr Val Leu Ser Asn Leu Leu Asp Gly 245 250 255 | 768 |
| aac ttg caa ggt atg tta aac att tca caa cac caa tgc gta aaa aaa Asn Leu Gln Gly Met Leu Asn Ile Ser Gln His Gln Cys Val Lys Lys 260 265 270 | 816 |
| caa tgt cca caa aat tct gga tgt ttc aga cat tta gat gaa aga gaa Gln Cys Pro Gln Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu 275 280 285 | 864 |
| gaa tgt aaa tgt tta tta aat tac aaa caa gaa ggt gat aaa tgt gtt Glu Cys Lys Cys Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val 290 295 300 | 912 |
| gaa aat cca aat cct act tgt aac gaa aat aat ggt gga tgt gat gca Glu Asn Pro Asn Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala 305 310 315 320 | 960 |
| gat gcc aaa tgt acc gaa gaa gat tca ggt agc aac gga aag aaa atc Asp Ala Lys Cys Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile 325 330 335 | 1008 |
| aca tgt gaa tgt act aaa cct gat tct tat cca ctt ttc gat ggt att Thr Cys Glu Cys Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile 340 345 350 | 1056 |
| ttc tgc agt cac cac cac cac cac cac taact Phe Cys Ser His His His His His His 355 360 | 1088 |

<210> 3

<211> 88

<212> DNA

<213> preferably, a bacterium, virus, or parasite

<400> 3

tcgacgagag ccatgaaggt cctcatcctt gcctgtctgg tggctctggc cattgcaaga
gagcaggaag aactcaatgt agtcggtta

60

88

<210> 4

<211> 88

<212> DNA

<213> preferably, a bacterium, virus, or parasite

B1
cont

<400> 4
 gatctaccga ctacattgag ttcttctctgc tctcttgcaa tggccagagc caccagacag 60
 gcaaggatga ggaccttcat ggctctcg 88

<210> 5
 <211> 60
 <212> DNA
 <213> preferably, a bacterium, virus, or parasite

<400> 5
 taactcgagc gaaccatgaa ggtcctcatc cttgcctgtc tgggtggctct ggccattgca 60

<210> 6
 <211> 48
 <212> DNA
 <213> preferably, a bacterium, virus, or parasite

<400> 6
 aattctcgag ttagtggtgg tgggtgggtg gactgcagaa ataccatc 48

<210> 7
 <211> 31
 <212> DNA
 <213> preferably, a bacterium, virus, or parasite

<400> 7
 aatagatctg cagtaactcc ttccgtaatt g 31

<210> 8
 <211> 1142
 <212> DNA
 <213> preferably, a bacterium, virus, or parasite

<220>
 <221> CDS
 <222> (1)...(1128)

<400> 8
 atg aag gtc ctc ata att gcc tgt ctg gtg gct ctg gcc att gca gcc 48
 Met Lys Val Leu Ile Ile Ala Cys Leu Val Ala Leu Ala Ile Ala Ala
 1 5 10 15

gtc act ccc tcc gtc atc gat aac atc ctg tcc aag atc gag aac gag 96
 Val Thr Pro Ser Val Ile Asp Asn Ile Leu Ser Lys Ile Glu Asn Glu
 20 25 30

tac gag gtg ctg tac ctg aag ccc ctg gca gga gtc tac agg agc ctg 144
 Tyr Glu Val Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser Leu
 35 40 45

aag aag cag ctg gag aac aac gtg atg acc ttc aac gtg aac gtg aag 192
 Lys Lys Gln Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val Lys
 50 55 60

gat atc ctg aac agc agg ttc aac aag agg gag aac ttc aag aac gtg 240
 Asp Ile Leu Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn Val
 65 70 75 80

ctg gag agc gat ctg atc ccc tac aag gat ctg acc agc agc aac tac 288
 Leu Glu Ser Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn Tyr
 85 90 95

BiCont.

gtg gtc aaa gat ccc tac aag ttc ctg aac aag gag aag aga gat aag 336
 Val Val Lys Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp Lys
 100 105 110

ttc ctg agc agt tac aat tac atc aag gat agc att gac acc gat atc 384
 Phe Leu Ser Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp Ile
 115 120 125

aac ttc gcc aac gat gtc ctg gga tac tac aag atc ctg tcc gag aag 432
 Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu Lys
 130 135 140

tac aag agc gat ctg gat agc atc aag aag tac atc aac gat aag cag 480
 Tyr Lys Ser Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys Gln
 145 150 155 160

gga gag aac gag aag tac ctg ccc ttc ctg aac aac atc gag acc ctg 528
 Gly Glu Asn Glu Lys Tyr Leu Pro Phe Leu Asn Asn Ile Glu Thr Leu
 165 170 175

tac aag acc gtc aac gat aag att gat ctg ttc gtg atc cac ctg gag 576
 Tyr Lys Thr Val Asn Asp Lys Ile Asp Leu Phe Val Ile His Leu Glu
 180 185 190

gcc aag gtc ctg cag tac aca tat gag aag agc aac gtg gag gtc aag 624
 Ala Lys Val Leu Gln Tyr Thr Tyr Glu Lys Ser Asn Val Glu Val Lys
 195 200 205

atc aag gag ctg aat tac ctg aag acc atc cag gat aag ctg gcc gat 672
 Ile Lys Glu Leu Asn Tyr Leu Lys Thr Ile Gln Asp Lys Leu Ala Asp
 210 215 220

ttc aag aag aac aac aac ttc gtc gga atc gcc gat ctg agc acc gat 720
 Phe Lys Lys Asn Asn Asn Phe Val Gly Ile Ala Asp Leu Ser Thr Asp
 225 230 235 240

tac aac cac aac aac ctg ctg acc aag ttc ctg agc acc gga atg gtc 768
 Tyr Asn His Asn Asn Leu Leu Thr Lys Phe Leu Ser Thr Gly Met Val
 245 250 255

ttc gaa aac ctg gcc aag acc gtc ctg agc aac ctg ctg gat gga aac 816
 Phe Glu Asn Leu Ala Lys Thr Val Leu Ser Asn Leu Leu Asp Gly Asn
 260 265 270

ctg cag gga atg ctg cag atc agc cag cac cag tgt gtg aag aag cag 864
 Leu Gln Gly Met Leu Gln Ile Ser Gln His Gln Cys Val Lys Lys Gln
 275 280 285

tgt ccc cag aac agc gga tgc ttc aga cac ctg gat gag agg gag gag 912
 Cys Pro Gln Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu Glu
 290 295 300

tgc aag tgc ctg ctg aac tac aag cag gaa gga gat aag tgt gtg gaa 960
 Cys Lys Cys Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu
 305 310 315 320

aac ccc aat cct act tgt aac gag aac aat gga gga tgc gat gcc gat 1008
 Asn Pro Asn Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp
 325 330 335

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7/10

gcc aag tgt acc gag gag gat tca gga agc aac gga aag aag atc acc 1056
Ala Lys Cys Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr
340 345 350

tgc gag tgt acc aag cct gat tct tat cca ctg ttc gat ggt att ttc 1104
Cys Glu Cys Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe
355 360 365

tgc agt cac cac cac cac cac cac taactcgagg atcc 1142
Cys Ser His His His His His His
370 375

<210> 9

<211> 82

<212> DNA

<213> preferably, a bacterium, virus, or parasite

<400> 9
ggcgcgtcga cgccaccatg aaggtcctca taattgctg tctggtggct ctggccattg 60
cagccgtcac tccctccgtc at 82

<210> 10

<211> 80

<212> DNA

<213> preferably, a bacterium, virus, or parasite

<400> 10
cgatgacgga gggagtgcgc gctgcaatgg ccagagccac cagacaggca attatgagga 60
ccttcattggt ggcgtcgagc 80

<210> 11

<211> 355

<212> PRT

<213> preferably, a bacterium, virus, or parasite

<400> 11
Ala Val Thr Pro Ser Val Ile Asp Asn Ile Leu Ser Lys Ile Glu Asn
1 5 10 15
Glu Tyr Glu Val Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser
20 25 30
Leu Lys Lys Gln Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val
35 40 45
Lys Asp Ile Leu Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn
50 55 60
Val Leu Glu Ser Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn
65 70 75 80
Tyr Val Val Lys Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp
85 90 95
Lys Phe Leu Ser Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp
100 105 110
Ile Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu
115 120 125
Lys Tyr Lys Ser Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys
130 135 140
Gln Gly Glu Asn Glu Lys Tyr Leu Pro Phe Leu Asn Asn Ile Glu Thr
145 150 155 160
Leu Tyr Lys Thr Val Asn Asp Lys Ile Asp Leu Phe Val Ile His Leu
165 170 175
Glu Ala Lys Val Leu Asn Tyr Thr Tyr Glu Lys Ser Asn Val Glu Val
180 185 190

Bent

Lys Ile Lys Glu Leu Asn Tyr Leu Lys Thr Ile Gln Asp Lys Leu Ala
 195 200 205
 Asp Phe Lys Lys Asn Asn Asn Phe Val Gly Ile Ala Asp Leu Ser Thr
 210 215 220
 Asp Tyr Asn His Asn Asn Leu Leu Thr Lys Phe Leu Ser Thr Gly Met
 225 230 235 240
 Val Phe Glu Asn Leu Ala Lys Thr Val Leu Ser Asn Leu Leu Asp Gly
 245 250 255
 Asn Leu Gln Gly Met Leu Asn Ile Ser Gln His Gln Cys Val Lys Lys
 260 265 270
 Gln Cys Pro Gln Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu
 275 280 285
 Glu Cys Lys Cys Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val
 290 295 300
 Glu Asn Pro Asn Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala
 305 310 315 320
 Asp Ala Lys Cys Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile
 325 330 335
 Thr Cys Glu Cys Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile
 340 345 350
 Phe Cys Ser
 355

<210> 12
 <211> 361
 <212> PRT
 <213> preferably, a bacterium, virus, or parasite

<400> 12
 Ala Val Thr Pro Ser Val Ile Asp Asn Ile Leu Ser Lys Ile Glu Asn
 1 5 10 15
 Glu Tyr Glu Val Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser
 20 25 30
 Leu Lys Lys Gln Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val
 35 40 45
 Lys Asp Ile Leu Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn
 50 55 60
 Val Leu Glu Ser Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn
 65 70 75 80
 Tyr Val Val Lys Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp
 85 90 95
 Lys Phe Leu Ser Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp
 100 105 110
 Ile Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu
 115 120 125
 Lys Tyr Lys Ser Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys
 130 135 140
 Gln Gly Glu Asn Glu Lys Tyr Leu Pro Phe Leu Asn Asn Ile Glu Thr
 145 150 155 160
 Leu Tyr Lys Thr Val Asn Asp Lys Ile Asp Leu Phe Val Ile His Leu
 165 170 175
 Glu Ala Lys Val Leu Asn Tyr Thr Tyr Glu Lys Ser Asn Val Glu Val
 180 185 190
 Lys Ile Lys Glu Leu Asn Tyr Leu Lys Thr Ile Gln Asp Lys Leu Ala
 195 200 205
 Asp Phe Lys Lys Asn Asn Asn Phe Val Gly Ile Ala Asp Leu Ser Thr
 210 215 220
 Asp Tyr Asn His Asn Asn Leu Leu Thr Lys Phe Leu Ser Thr Gly Met
 225 230 235 240
 Val Phe Glu Asn Leu Ala Lys Thr Val Leu Ser Asn Leu Leu Asp Gly
 245 250 255

Asn Leu Gln Gly Met Leu Asn Ile Ser Gln His Gln Cys Val Lys Lys
 260 265 270
 Gln Cys Pro Gln Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu
 275 280 285
 Glu Cys Lys Cys Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val
 290 295 300
 Glu Asn Pro Asn Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala
 305 310 315 320
 Asp Ala Lys Cys Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile
 325 330 335
 Thr Cys Glu Cys Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile
 340 345 350
 Phe Cys Ser His His His His His His
 355 360

<210> 13

<211> 376

<212> PRT

<213> preferably, a bacterium, virus, or parasite

<400> 13

Met Lys Val Leu Ile Ile Ala Cys Leu Val Ala Leu Ala Ile Ala Ala
 1 5 10 15
 Val Thr Pro Ser Val Ile Asp Asn Ile Leu Ser Lys Ile Glu Asn Glu
 20 25 30
 Tyr Glu Val Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser Leu
 35 40 45
 Lys Lys Gln Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val Lys
 50 55 60
 Asp Ile Leu Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn Val
 65 70 75 80
 Leu Glu Ser Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn Tyr
 85 90 95
 Val Val Lys Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp Lys
 100 105 110
 Phe Leu Ser Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp Ile
 115 120 125
 Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu Lys
 130 135 140
 Tyr Lys Ser Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys Gln
 145 150 155 160
 Gly Glu Asn Glu Lys Tyr Leu Pro Phe Leu Asn Asn Ile Glu Thr Leu
 165 170 175
 Tyr Lys Thr Val Asn Asp Lys Ile Asp Leu Phe Val Ile His Leu Glu
 180 185 190
 Ala Lys Val Leu Gln Tyr Thr Tyr Glu Lys Ser Asn Val Glu Val Lys
 195 200 205
 Ile Lys Glu Leu Asn Tyr Leu Lys Thr Ile Gln Asp Lys Leu Ala Asp
 210 215 220
 Phe Lys Lys Asn Asn Asn Phe Val Gly Ile Ala Asp Leu Ser Thr Asp
 225 230 235 240
 Tyr Asn His Asn Asn Leu Leu Thr Lys Phe Leu Ser Thr Gly Met Val
 245 250 255
 Phe Glu Asn Leu Ala Lys Thr Val Leu Ser Asn Leu Leu Asp Gly Asn
 260 265 270
 Leu Gln Gly Met Leu Gln Ile Ser Gln His Gln Cys Val Lys Lys Gln
 275 280 285
 Cys Pro Gln Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu Glu
 290 295 300
 Cys Lys Cys Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu
 305 310 315 320

Book

Panel.
